



VERIFICATION SUMMARY

PATENT APPLICATION: US/10/088,548

DATE: 04/12/2002 TIME: 09:26:43

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\04122002\J088548.raw

 $L:8\ M:270\ C:$ Current Application Number differs, Replaced Current Application No

L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE

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12	
C staff)	
)	
90	

Number:	_	1	1)(<u>08</u>	8,)	<u></u>							_									Proceed by:		ng	Date	<u>"</u> —		121	
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Other:																															
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CRF ors Corrected by the STIC System Branch

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



PCT10

RAW SEQUENCE LISTING DATE: 04/12/2002 PATENT APPLICATION: US/10/088,548 TIME: 09:26:42

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\04122002\J088548.raw

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4 <110> APPLICANT: Mogam Biotechnology Research Institute et al
 6 <120> TITLE OF INVENTION: A NOVEL ANGIOGENESIS INHIBITOR
 8 <140> CURRENT APPLICATION NUMBER: US/10/088,548
 8 <141> CURRENT FILING DATE: 2002-03-15
 0 <130> FILE REFERENCE:
 8 <160> NUMBER OF SEQ ID NOS: 14
10 <170> SOFTWARE: KOPATIN 1.5
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13 <211> LENGTH: 924
14 <212> TYPE: DNA
15 <213> ORGANISM: Homo sapiens
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20 tecaceaetg teacaggaag gacetgteaa tettggteat etatgatace acaetggeat
                                                                           120
22 cagaggaccc cagaaaacta cccaaatgct ggcctgaccg agaactactg caggaatcca
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24 gattctggga aacaaccctg gtgttacaca accgatccgt gtgtgaggtg ggagtactgc
                                                                           240
26 aatctgacac aatgctcaga aacagaatca ggtgtcctag agactcccac tgttgttcca
                                                                           300
28 gttccaagca tggaggetca ttctgaagca gcaccaactg agcaaacccc tgtggtccgc
                                                                           360
30 cagtgctacc atggcaatgg ccagagttat cgaggcacat tctccaccac tgtcacagga
                                                                           420
32 aggacatgte aatettggte atecatgaca ceacacegge ateagaggae eecagaaaae
                                                                           480
34 tacccaaatg atggcctgac aatgaactac tgcaggaatc cagatgccga tacaggccct
                                                                           540
36 tggtgtttta ccacggaccc cagcatcagg tgggagtact gcaacctgac gcgatgctca
                                                                           600
38 gacacagaag ggactgtggt cgctcctccg actgtcatcc aggttccaag cctagggcct
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40 cettetgaae aagaetgtat gtttgggaat gggaaaggat aceggggeaa gaaggeaace
                                                                           720
42 actgttactg ggacgccatg ccaggaatgg gctgcccagg agccccatag acacagcacg
                                                                           780
44 ttcattccag ggacaaataa atgggcaggt ctggaaaaaa attactgccg taaccctgat
                                                                           840
46 ggtgacatca atggtccctg gtgctacaca atgaatccaa gaaaactttt tgactactgt
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48 gatatecete tetgtgeate etet
                                                                           924
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52 <211> LENGTH: 308
53 <212> TYPE: PRT
54 <213> ORGANISM: Homo sapiens
56 <400> SEQUENCE: 2
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58
     1
                     5
60 Arg Gly Ile Ser Ser Thr Thr Val Thr Gly Arg Thr Cys Gln Ser Trp
61
                20
                                    25
63 Ser Ser Met Ile Pro His Trp His Gln Arg Thr Pro Glu Asn Tyr Pro
66 Asn Ala Gly Leu Thr Glu Asn Tyr Cys Arg Asn Pro Asp Ser Gly Lys
                            55
```

69 Gln Pro Trp Cys Tyr Thr Thr Asp Pro Cys Val Arg Trp Glu Tyr Cys

70

70

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72 Asn Leu Thr Gln Cys Ser Glu Thr Glu Ser Gly Val Leu Glu Thr Pro 73 90 95	
75 Thr Val Val Pro Val Pro Ser Met Glu Ala His Ser Glu Ala Ala Pro 76 100 105 110	
78 Thr Glu Gln Thr Pro Val Val Arg Gln Cys Tyr His Gly Asn Gly Gln 79 115 120 125	
81 Ser Tyr Arg Gly Thr Phe Ser Thr Thr Val Thr Gly Arg Thr Cys Gln 82 130 135 140	
84 Ser Trp Ser Ser Met Thr Pro His Arg His Gln Arg Thr Pro Glu Asn 85 145 150 155 160	
87 Tyr Pro Asn Asp Gly Leu Thr Met Asn Tyr Cys Arg Asn Pro Asp Ala 88 165 170 175	
90 Asp Thr Gly Pro Trp Cys Phe Thr Thr Asp Pro Ser Ile Arg Trp Glu 91 180 185 190	
93 Tyr Cys Asn Leu Thr Arg Cys Ser Asp Thr Glu Gly Thr Val Val Ala 94 195 200 205	
96 Pro Pro Thr Val Ile Gln Val Pro Ser Leu Gly Pro Pro Ser Glu Gln 97 210 215 220	
99 Asp Cys Met Phe Gly Asn Gly Lys Gly Tyr Arg Gly Lys Lys Ala Thr 100 225 230 235 240	
100 225 240 102 Thr Val Thr Gly Thr Pro Cys Gln Glu Trp Ala Ala Gln Glu Pro His	
103 245 250 255	
105 Arg His Ser Thr Phe Ile Pro Gly Thr Asn Lys Trp Ala Gly Leu Glu	
106 260 265 270	
108 Lys Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ile Asn Gly Pro Trp Cys 109 275 280 285	
111 Tyr Thr Met Asn Pro Arg Lys Leu Phe Asp Tyr Cys Asp Ile Pro Leu	
112 290 295 300	
114 Cys Ala Ser Ser	
115 305	
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128 cagaggaccc cagaaaacta cccaaatgct ggcctgaccg agaactactg caggaatcca	180
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141 Lys Ser Pro Val Val Gln Asp Cys Tyr His Gly Asp Gly Arg Ser Tyr	
142 1 5 10 15	
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145 20 25 30	



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DATE: 04/12/2002 TIME: 09:26:42

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. 147 . 148	Ser Ser Met Ile Pro His Trp His Gln Arg Thr Pro Glu Asn Tyr Pro 35 40 45	
150	Asn Ala Gly Leu Thr Glu Asn Tyr Cys Arg Asn Pro Asp Ser Gly Lys	
151	50 55 60	
	Gln Pro Trp Cys Tyr Thr Thr Asp Pro Cys Val Arg Trp Glu Tyr Cys	
154	65 70 75 80	
	Asn Leu Thr Gln Cys Ser Glu Thr Glu Ser Gly	
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	<400> SEQUENCE: 5	
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	acaggaagga catgtcaatc ttggtcatcc atgacaccac accggcatca gaggacccca	120
	gaaaactacc caaatgatgg cctgacaatg aactactgca ggaatccaga tgccgataca	180
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184	1 5 10 15	
186	Ser Thr Thr Val Thr Gly Arg Thr Cys Gln Ser Trp Ser Ser Met Thr	
187	20 25 30	
	Pro His Arg His Gln Arg Thr Pro Glu Asn Tyr Pro Asn Asp Gly Leu	
190	35 40 45	
	Thr Met Asn Tyr Cys Arg Asn Pro Asp Ala Asp Thr Gly Pro Trp Cys	
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	Phe Thr Thr Asp Pro Ser Ile Arg Trp Glu Tyr Cys Asn Leu Thr Arg	
196	65 70 75 80 Cys Ser Asp Thr Glu Gly Thr Val Val	
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	<211> LENGTH: 258	
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	ccagggacaa ataaatgggc aggtctggaa aaaaattact gccgtaaccc tgatggtgac	180
214	atcaatggtc cctggtgcta cacaatgaat ccaagaaaac tttttgacta ctgtgatatc	240
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Input Set : A:\PTO.DC.txt

224	<400>	SEQUE	NCE:	8												
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226		-	-	5		-		_	10	-	-	_	_	15		
		hr Thr	Val	Thr	Gly	Thr	Pro	Cys	Gln	Glu	Trp	Ala	Ala	Gln	Glu	
229			20		-			25					30			
231	Pro H	is Arg	His	Ser	Thr	Phe	Ile	Pro	Gly	Thr	Asn	Lys	Trp	Ala	Gly	
232		35					40		-			45	~		•	
234	Leu G	lu Lys	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ile	Asn	Gly	Pro	
235		50				55			_	_	60			_		
237	Trp C	ys Tyr	Thr	Met	Asn	${\tt Pro}$	Arg	Lys	Leu	Phe	Asp	Tyr	Cys	Asp	Ile	
238	65				70					75					80	
240	Pro Le	eu Cys	Ala	Ser	Ser											
241				85												
244	<210>	SEQ II	ON C	: 9												
245	<211>	LENGT	H: 29	9												
		TYPE:														
247	<213>	ORGANI	ISM:	Arti	ifici	al S	Seque	ence								
249	<220>	FEATUR	RE:													
		OTHER			:NOI	sir	igle	star	nded	olig	gonuc	cleot	cide			
		SEQUE														
		atgaa a			g gt	cca	gat									29
		SEQ II														
		LENGT		3												
		TYPE:														
		ORGANI		Arti	fici	al S	Seque	ence								
		FEATUR														
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		LENGTE		L												
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		SEQ II														
		LENGTE)												
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		LENGTH														
		TYPE:		,												
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PATENT APPLICATION: US/10/088,548

DATE: 04/12/2002 TIME: 09:26:42

Input Set : A:\PTO.DC.txt

297 <220> FI	EATURE:	
298 <223> 05	THER INFORMATION: single stranded oligonucleotide	
300 <400> SI	EQUENCE: 13	
301 cgggatco	ctt agaccacagt cccttc	26
304 <210> SI	EQ ID NO: 14	
305 <211> LI	ENGTH: 23	
306 <212> TY	YPE: DNA	
307 <213> OF	RGANISM: Artificial Sequence	
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313 cgggatco	ctt aagaggatgc aca	23